

SEQUENCE LISTING

<110> POWDERJECT RESEARCH LIMITED AND GLAXO GROUP LIMITED

<120> ADJUVANT

<130> N.88232 GCW

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> HBsAg in BLAB/C mice

<400> 1

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<210> 2

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> HSV CD8 in BLAB/C mice

<400> 2

His Gly Pro Ser Leu Tyr Arg Thr Phe

1

5

&lt;210&gt; 3

&lt;211&gt; 1503

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleotide sequence of p55 gag insert in pGagOptrpr2

&lt;400&gt; 3

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cagatgggttc atcaggccat cagcccccg gacgtcaatg cctgggtgaa ggttgtcgaa      480
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tataagacc tgcgagcaga gcaggcctct caggaggtca aaaactggat gacggagaca      960
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gccaccctgg aagagatgat gaccgcctgt cagggagtag gcggaccggg acacaaagcc     1080
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accgcccgca actgtcgggc cctaggaag aaaggggtgtt ggaagtgcgg caaggagga     1260
caccagatga aagactgtac agaacgacag gccaattttc ttggaaagat ttggccgagc     1320

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aaggagctgt accctttaac ttctctgcgt tctctctttg gcaacgaccc gtcgtctcaa 1500  
taa 1503

<210> 4

<211> 500

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of p55 gag insert in pGagOptrpr2

<400> 4

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp  
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys  
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro  
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu  
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn  
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp  
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys  
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val  
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His  
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu  
 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser  
 165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly  
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu  
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala  
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr  
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile  
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys  
 260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly  
 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu  
 290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr  
 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala  
 325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly  
 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser  
 355 360 365

Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg  
 370 375 380

Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His  
385 390 395 400

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys  
405 410 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn  
420 425 430

Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe  
435 440 445

Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg  
450 455 460

Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp  
465 470 475 480

Lys Glu Leu Tyr Pro Leu Thr Ser Leu Arg Ser Leu Phe Gly Asn Asp  
485 490 495

Pro Ser Ser Gln  
500

<210> 5

<211> 1515

<212> DNA

<213> Artificial sequence

<220>

<223> nucleotide sequence of the p17/24trNEF insert in p17/24trNEF1

<400> 5

|                                                                   |     |
|-------------------------------------------------------------------|-----|
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| ttaaggccag ggggaaagaa aaaatataaa ttaaaacata tagtatgggc aagcagggag | 120 |
| ctagaacgat tcgcagttaa tcttggcctg ttagaaacat cagaaggctg tagacaaata | 180 |
| ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat | 240 |
| acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct | 300 |
| ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct | 360 |
| gacacaggac acagcaatca ggtcagccaa aattacccta tagtgcagaa catccagggg | 420 |

caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480  
 gagaaggctt tcagcccaga agtgataccc atgttttcag cattatcaga aggagccacc 540  
 ccacaagatt taaacaccat gctaaacaca gtggggggac atcaagcagc catgcaaag 600  
 ttaaaagaga ccatcaatga ggaagctgca gaatgggata gagtgcaccc agtgcatgca 660  
 gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720  
 agtacccttc aggaacaaat aggatggatg acaaataatc cacctatccc agtaggagaa 780  
 atttataaaa gatggataat cctgggatta aataaaatag taagaatgta tagccctacc 840  
 agcattctgg acataagaca aggacaaaa gaacccttta gagactatgt agaccggttc 900  
 tataaaactc taagagccga gcaagcttca caggaggtaa aaaattggat gacagaaacc 960  
 ttgttggtcc aaaatgcgaa ccagattgt aagactatct taaaagcatt gggaccagcg 1020  
 gctacactag aagaaatgat gacagcatgt caggagtag gaggaccgga ccataaggca 1080  
 agagttttgg tgggttttcc agtcacacct caggtaacct taagaccaat gacttacaag 1140  
 gcagctgtag atcttagcca ctttttaaaa gaaaaggggg gactggaagg gctaattcac 1200  
 tcccaaagaa gacaagatat ccttgatctg tggatctacc acacacaagg ctacttcct 1260  
 gattggcaga actacacacc agggccaggg gtcagatatc cactgacctt tggatggtgc 1320  
 tacaagctag taccagttga gccagataag gtagaagagg ccaataaagg agagaacacc 1380  
 agcttggtac accctgtgag cctgcatggg atggatgacc cggagagaga agtggttagag 1440  
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 ttcaagaact gctga 1515

<210> 6

<211> 504

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of the p17/24trNEF insert in p17/24trNEF1

<400> 6

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp  
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys  
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro  
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu  
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn  
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp  
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys  
 100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val  
 115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His  
 130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu  
 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser  
 165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly  
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu  
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala  
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr  
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile  
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys  
 260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly  
 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu  
 290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr  
 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala  
 325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly  
 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Val Gly Phe Pro Val  
 355 360 365

Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp  
 370 375 380

Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His  
 385 390 395 400

Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln  
 405 410 415

Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg  
 420 425 430

Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro  
 435 440 445

Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His  
 450 455 460

Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu  
 465 470 475 480

Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu Leu  
 485 490 495

His Pro Glu Tyr Phe Lys Asn Cys  
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<210> 7

<211> 1518

<212> DNA

<213> Artificial sequence

<220>

<223> nucleotide sequence of the p17/24opt/trNef insert in p17/24opt/trNef1

<400> 7

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cttgaacggt ttgccgtgaa cccaggcctg ctggaaacat ctgagggatg tcgccagatc      180
ctggggcaat tgcagccatc cctccagacc gggagtgaag agctgaggtc cttgtataac      240
acagtggcta ccctctactg cgtacaccag aggatcgaga ttaaggatac caaggaggcc      300
ttggacaaaa ttgaggagga gcaaaacaag agcaagaaga aggccagca ggcagctgct      360
gacactgggc atagcaacca ggtatcacag aactatccta ttgtccaaaa cattcagggc      420
cagatggttc atcaggccat cagcccccg agctcaatg cctgggtgaa ggttgtcgaa      480
gagaaggcct tttctcctga ggttatcccc atgttctccg ctttgagtga gggggccact      540
cctcaggacc tcaatacaat gcttaatacc gtggggggcc atcaggccgc catgcaaag      600
ttgaaggaga ctatcaacga ggaggcagcc gagtgggaca gagtgcattc cgtccacgct      660
ggcccaatcg cgcccgga gatgcgggag cctcgcggt ctgacattgc cggcaccacc      720
tctacactgc aagagcaa atcgatggatg accaacaatc ctcccatccc agttggagaa      780
atctataaac ggtggatcat tctcggtctc aataaaattg ttagaatgta ctctccgaca      840
tccatccttg acattagaca gggacccaaa gagcctttta gggattacgt cgaccggttt      900
tataagaccc tgcgagcaga gcaggcctct caggaggtca aaaactggat gacggagaca      960
ctcctggtac agaacgctaa ccccgactgc aaaacaatct tgaaggcact aggcccggt      1020
gccaccctgg aagagatgat gaccgcctgt caggggagtag gcggaccggg acacaaagcc      1080
agagtgttga tggtgggttt tccagtcaca cctcaggtag ctttaagacc aatgacttac      1140
aaggcagctg tagatcttag ccacttttta aaagaaaagg ggggactgga agggctaatt      1200
cactcccaaa gaagacaaga tctccttgat ctgtggatct accacacaca aggctacttc      1260
cctgattggc agaactacac accagggcca ggggtcagat atccactgac ctttggatgg      1320
tgctacaagc tagtaccagt tgagccagat aaggtagaag aggcccaataa aggagagaac      1380
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accagcttgt tacaccctgt gagcctgcat gggatggatg acccgagag agaagtgtta 1440  
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 tacttcaaga actgctga 1518

<210> 8

<211> 505

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of the p17/24opt/trNef insert in p17/24opt/trNef1

<400> 8

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys  
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro  
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu  
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn  
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp  
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys  
 100 105 110

Lys Lys Ala Gln Gln Ala Ala Asp Thr Gly His Ser Asn Gln Val  
 115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His  
 130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu  
 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser  
 165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly  
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu  
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala  
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr  
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile  
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys  
 260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly  
 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu  
 290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr  
 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala  
 325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly  
 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Val Gly Phe Pro  
 355 360 365

Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val  
 370 375 380

Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile

385

390

395

400

His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr  
 405 410 415

Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val  
 420 425 430

Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu  
 435 440 445

Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu  
 450 455 460

His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu  
 465 470 475 480

Glu Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu  
 485 490 495

Leu His Pro Glu Tyr Phe Lys Asn Cys  
 500 505

&lt;210&gt; 9

&lt;211&gt; 1689

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; nucleotide sequence of RT insert of p7077-RT3

&lt;400&gt; 9

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 cccaagggtca agcagtggcc actcaccgag gagaagatca aggccctggg ggagatctgc 120  
 accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaacct atacaacacc 180  
 cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggg ggatttccgg 240  
 gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc 300  
 ggctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc 360  
 cctctggagc aggacttttag aaagtacacc gcctttacca tcccatctat caacaacgag 420  
 acccctggca tcagatatca gtacaacgtc ctccccagg gctggaaggg ctctcccgcc 480

|                                                                    |      |
|--------------------------------------------------------------------|------|
| atthttccaga gctccatgac caagatcctg gagccgtttc ggaagcagaa ccccgatata | 540  |
| gtcatctacc agtacatgga cgacctgtac gtgggctctg acctggaaat cgggcagcat  | 600  |
| cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac  | 660  |
| aagaagcatc agaaggagcc gccattcctg tggatgggct acgagctcca tcccgacaag  | 720  |
| tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag  | 780  |
| aagctggtgg gcaagctcaa ctgggctagc cagatctata ccgggatcaa ggtgcgccag  | 840  |
| ctctgcaagc tgctgcgcgg caccaaggcc ctgaccgagg tgattcccct cacggaggaa  | 900  |
| gccgagctcg agctggctga gaaccgggag atcctgaagg agcccgtgca cggcgtgtac  | 960  |
| tatgaccctt ccaaggacct gatcgccgaa atccagaagc agggccaggg gcagtggaca  | 1020 |
| taccagattt accaggagcc tttcaagaac ctcaagaccg gcaagtacgc ccgcatgagg  | 1080 |
| ggcgcccaca ccaacgatgt caagcagctg accgaggccg tccagaagat cacgaccgag  | 1140 |
| tccatcgtga tctgggggaa gacaccaag ttcaagctgc ctatccagaa ggagacctgg   | 1200 |
| gagacgtggt ggaccgaata ttggcaggcc acctggattc ccgagtggga gttcgtgaat  | 1260 |
| acacctctc tggatgaagct gtggtaccag ctcgagaagg agcccatcgt gggcgcgag   | 1320 |
| acattctacg tggacggcgc ggccaaccgc gaaacaaagc tcgggaaggc cgggtacgtc  | 1380 |
| accaaccggg gccgcagaa ggtcgtcacc ctgaccgaca ccaccaacca gaagacggag   | 1440 |
| ctgcaggcca tctatctcgc tctccaggac tccggcctgg aggtgaacat cgtgacggac  | 1500 |
| agccagtacg cgctgggcat tattcaggcc cagccggacc agtccgagag cgaactggtg  | 1560 |
| aaccagatta tcgagcagct gatcaagaaa gagaaggctt acctcgctg ggtcccgcc    | 1620 |
| cataagggca ttggcggcaa cgagcaggtc gacaagctgg tgagtgcggg gattagaaag  | 1680 |
| gtgctgtaa                                                          | 1689 |

<210> 10

<211> 562

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of RT insert of p7077-RT3

<400> 10

Met Gly Pro Ile Ser Pro Ile Glu Thr Val Ser Val Lys Leu Lys Pro

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys | 20  | 25  | 30  |
| Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys | 35  | 40  | 45  |
| Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala | 50  | 55  | 60  |
| Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg | 65  | 70  | 75  |
| Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile | 85  | 90  | 95  |
| Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp | 100 | 105 | 110 |
| Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys | 115 | 120 | 125 |
| Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile | 130 | 135 | 140 |
| Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala | 145 | 150 | 155 |
| Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln | 165 | 170 | 175 |
| Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly | 180 | 185 | 190 |
| Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg | 195 | 200 | 205 |
| Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln | 210 | 215 | 220 |
| Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys | 225 | 230 | 235 |
| Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val | 245 | 250 | 255 |

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile  
260 265 270

Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr  
275 280 285

Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu  
290 295 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr  
305 310 315 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln  
325 330 335

Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys  
340 345 350

Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys  
355 360 365

Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile  
370 375 380

Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp  
385 390 395 400

Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp  
405 410 415

Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu  
420 425 430

Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala  
435 440 445

Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly  
450 455 460

Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu  
465 470 475 480

Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn  
485 490 495

Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro  
500 505 510

Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile  
515 520 525

Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile  
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Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys  
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Val Leu

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<220>

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| accgagatgg agaaagaggg caagatcagc aagatcgggc ctgagaacct atacaacacc  | 180 |
| cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttccgg  | 240 |
| gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc  | 300 |
| ggcctgaaga agaagaagag cgtgaccgtg ctggacgtgg gcgacgctta cttcagcgtc  | 360 |
| cctctggacg aggactttag aaagtacacc gcctttacca tcccatctat caacaacgag  | 420 |
| acctctggca tcagatatca gtacaacgtc ctccccagg gctggaaggg ctctcccgcc   | 480 |
| atcttccaga gctccatgac caagatcctg gagccgtttc ggaagcagaa ccccgatctc  | 540 |
| gtcatctacc agtacatgga cgacctgtac gtgggctctg acctggaaat cgggcagcat  | 600 |
| cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac  | 660 |
| aagaagcatc agaaggagcc gccattcctg tggatgggct acgagctcca tcccagacaag | 720 |
| tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag  | 780 |



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<210> 12

<211> 562

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of the coding insert in p73i-RT3

<400> 12

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Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala  
 50 55 60

Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg  
 65 70 75 80

Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile  
 85 90 95

Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp  
 100 105 110

Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys  
 115 120 125

Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile  
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Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala  
 145 150 155 160

Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln  
 165 170 175

Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly  
 180 185 190

Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg  
 195 200 205

Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln  
 210 215 220

Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys  
 225 230 235 240

Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val  
 245 250 255

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile  
 260 265 270

Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr  
 275 280 285

Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu  
290 295 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr  
305 310 315 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln  
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Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys  
340 345 350

Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys  
355 360 365

Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile  
370 375 380

Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp  
385 390 395 400

Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp  
405 410 415

Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu  
420 425 430

Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala  
435 440 445

Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly  
450 455 460

Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu  
465 470 475 480

Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn  
485 490 495

Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro  
500 505 510

Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile  
515 520 525

Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile  
530 535 540

Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys  
545 550 555 560

Val Leu